

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: KLEIN, Michel H
DU, Run-Pan
EWASYSHYN, Mary E

(ii) TITLE OF INVENTION: INFECTION DETECTION METHOD USING CHIMERIC PROTEIN

(iii) NUMBER OF SEQUENCES: 38

(iv) CORRESPONDENCE ADDRESS:
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 (C) CITY: Toronto
 (D) STATE: Ontario
 (E) COUNTRY: Canada
 (F) ZIP: M5G 1R7

(v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
 (A) APPLICATION NUMBER:
 (B) FILING DATE:
 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: US 08/467,961
 (B) FILING DATE: 06-JUN-1995

(vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: US 08/001,554
 (B) FILING DATE: 06-JAN-1993

(vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: GB 9200117.1
 (B) FILING DATE: 06-JAN-1992

(viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: STEWART, Michael I
 (B) REGISTRATION NUMBER: 24,973
 (C) REFERENCE/DOCKET NUMBER: 1038-1000 MIS:jb

(ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: (416) 595-1155
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)

AAGTCAATAC	CAACAAC'TAT	TAGCAGTCAT	ACGTGCAAGA	ACAAGAAAGA	AGAGATTCAA	60
AAAGCTAAAT	AAGAGAAATC	AAAACAAAAG	GTATAGAACA	CCCGAACAAC	AAAATCAAAA	120
CATCCAATCC	ATTTTAAACA	AAAATTCCAA	AAGAGACCGG	CAACACAACA	AGCACCAAAC	180
ACAATGCCAA	CTTTAATACT	GCTAATTATT	ACAACAATGA	TTATGGCATC	TTCCTGCCAA	240
ATAGATATCA	CAAAACTACA	GCATGTAGGT	GTATTGGTCA	ACAGTCCCAA	AGGGATGAAG	300
ATATCACAAA	ACTTCGAAAC	AAGATATCTA	ATTTTGTAGCC	TCATACCAAA	AATAGAAGAC	360
TCTAACTCTT	GTGGTGACCA	ACAGATCAAA	CAATACAAGA	GGTTATTGGA	TAGACTGATC	420
ATCCCTCTAT	ATGATGGATT	AAGATTACAG	AAAGATGTGA	TAGTAACCAA	TCAAGAATCC	480
AATGAAAACA	CTGATCCCAG	AACAAGACGA	TCCTTTGGAG	GGGTAATTGG	AACCATTGCT	540
CTGGGAGTAG	CAACCTCAGC	ACAAATTACA	GCGGCAGTTG	CTCTGGTTGA	AGCCAAGCAG	600
GCAAAATCAG	ACATCGAAAA	ACTCAAAGAA	GCAATCAGGG	ACACAAACAA	AGCAGTGCAG	660
TCAGTTCAGA	GCTCTATAGG	AAATTTAATA	GTAGCAATTA	AATCAGTCCA	AGATTATGTC	720
AACAACGAAA	TGGTGCCATC	GATTGCTAGA	CTAGGTTGTG	AAGCAGCAGG	ACTTCAATTA	780
GGAATTGCAT	TAACACAGCA	TTACTCAGAA	TTAACAAACA	TATTTGGTGA	TAACATAGGA	840
TCGTTACAAG	AAAAAGGAAT	AAAATTACAA	GGTATAGCAT	CATTATACCG	CACAAATATC	900
ACAGAAATAT	TCACAACATC	AACAGTTGAT	AAATATGATA	TCTATGATCT	ATTATTTACA	960
GAATCAATAA	AGGTGAGAGT	TATAGATGTT	GATTTGAATG	ATTACTCAAT	CACCCCTCCAA	1020
GTCAGACTCC	CTTTATTTAAC	TAGGCTGCTG	AACACTCAGA	TCTACAAAGT	AGATTCCATA	1080
TCATATAATA	TCCAAAACAG	AGAATGGTAT	ATCCCTCTTC	CCAGCCATAT	CATGACGAAA	1140
GGGGCATTTT	TAGGTGGAGC	AGATGTCAAG	GAATGTATAG	AAGCATTCAG	CAGTTATATA	1200
TGCCCTTCTG	ATCCAGGATT	TGTACTAAAC	CATGAAATGG	AGAGCTGCTT	ATCAGGAAAC	1260
ATATCCCAAT	GTCCAAGAAC	CACGGTCACA	TCAGACATTG	TTCCAAGATA	TGCATTTGTC	1320
AATGGAGGAG	TGGTTGCAAA	CTGTATAACA	ACCACCTGTA	CATGCAACGG	AATCGACAAT	1380

145				150					155					160		
Val	Gln	Ser	Ser	Ile	Gly	Asn	Leu	Ile	Val	Ala	Ile	Lys	Ser	Val	Gln	
				165					170					175		
Asp	Tyr	Val	Asn	Asn	Glu	Ile	Val	Pro	Ser	Ile	Ala	Arg	Leu	Gly	Cys	
				180					185					190		
Glu	Ala	Ala	Gly	Leu	Gln	Leu	Gly	Ile	Ala	Leu	Thr	Gln	His	Tyr	Ser	
				195					200					205		
Glu	Leu	Thr	Asn	Ile	Phe	Gly	Asp	Asn	Ile	Gly	Ser	Leu	Gln	Glu	Lys	
				210					215					220		
Gly	Ile	Lys	Leu	Gln	Gly	Ile	Ala	Ser	Leu	Tyr	Arg	Thr	Asn	Ile	Thr	
				225					230					235		
Glu	Ile	Phe	Thr	Thr	Ser	Thr	Val	Asp	Lys	Tyr	Asp	Ile	Tyr	Asp	Leu	
				245					250					255		
Leu	Phe	Thr	Glu	Ser	Ile	Lys	Val	Arg	Val	Ile	Asp	Val	Asp	Leu	Asn	
				260					265					270		
Asp	Tyr	Ser	Ile	Thr	Leu	Gln	Val	Arg	Leu	Pro	Leu	Leu	Thr	Arg	Leu	
				275					280					285		
Leu	Asn	Thr	Gln	Ile	Tyr	Lys	Val	Asp	Ser	Ile	Ser	Tyr	Asn	Ile	Gln	
				290					295					300		
Asn	Arg	Glu	Trp	Tyr	Ile	Pro	Leu	Pro	Ser	His	Ile	Met	Thr	Lys	Gly	
				305					310					315		
Ala	Phe	Leu	Gly	Gly	Ala	Asp	Val	Lys	Glu	Cys	Ile	Glu	Ala	Phe	Ser	
				325					330					335		
Ser	Tyr	Ile	Cys	Pro	Ser	Asp	Pro	Gly	Phe	Val	Leu	Asn	His	Glu	Met	
				340					345					350		
Glu	Ser	Cys	Leu	Ser	Gly	Asn	Ile	Ser	Gln	Cys	Pro	Arg	Thr	Thr	Val	
				355					360					365		
Thr	Ser	Asp	Ile	Val	Pro	Arg	Tyr	Ala	Phe	Val	Asn	Gly	Gly	Val	Val	
				370					375					380		
Ala	Asn	Cys	Ile	Thr	Thr	Thr	Cys	Thr	Cys	Asn	Gly	Ile	Asp	Asn	Arg	
				385					390					395		
Ile	Asn	Gln	Pro	Pro	Asp	Gln	Gly	Val	Lys	Ile	Ile	Thr	His	Lys	Glu	
				405					410					415		
Cys	Asn	Thr	Ile	Gly	Ile	Asn	Gly	Met	Leu	Phe	Asn	Thr	Asn	Lys	Glu	
				420					425					430		
Gly	Thr	Leu	Ala	Phe	Tyr	Thr	Pro	Asn	Asp	Ile	Thr	Leu	Asn	Asn	Ser	
				435					440					445		
Val	Ala	Leu	Asp	Pro	Ile	Asp	Ile	Ser	Ile	Glu	Leu	Asn	Lys	Ala	Lys	

1. *Phragmites australis* (Cav.) Trin. ex Steud.
 2. *Scirpus americanus* L.
 3. *Scirpus setaceus* L.
 4. *Scirpus robustus* L.
 5. *Scirpus subterminalis* L.
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 100. *Scirpus subterminalis* L.

TGATGAAAGA TCAGATTATG CATCATCAGG CATAGAAGAT ATTGTACTTG ATATTGTCAA	900
TTATGATGGC TCAATCTCAA CAACAAGATT TAAGAATAAT AACATAAGCT TTGATCAACC	960
TTATGCTGCA CTATACCCAT CTGTTGGACC AGGGATATAC TACAAAGGCA AAATAATATT	1020
TCTCGGGTAT GGAGGTCTTG AACATCCAAT AAATGAGAAT GTAATCTGCA ACACAACTGG	1080
GTGTCCCGGG AAAACACAGA GAGACTGCAA TCAGGCATCT CATAGTCCAT GGTTTTTCAGA	1140
TAGGAGGATG GTCAACTCTA TCATTGTTGT TGACAAAGGC TTAAACTCAA TTCCAAAATT	1200
GAAGGTATGG ACGATATCTA TGAGACAGAA TTACTGGGGG TCAGAAGGAA GGTTACTTCT	1260
ACTAGGTAAC AAGATCTATA TATATACAAG ATCCACAAGT TGGCATAGCA AGTTACAATT	1320
AGGAATAATT GATATTACTG ATTACAGTGA TATAAGGATA AAATGGACAT GGCATAATGT	1380
GCTATCAAGA CCAGGAAACA ATGAATGTCC ATGGGGACAT TCATGTCCAG ATGGATGTAT	1440
AACAGGAGTA TATACTGATG CATATCCACT CAATCCCACA GGGAGCATTG TGTCATCTGT	1500
CATATTAGAT TCACAAAAAT CGAGAGTGAA CCCAGTCATA ACTTACTCAA CAGCAACCGA	1560
AAGAGTAAAC GAGCTGGCCA TCCGAAACAG AACACTCTCA GCTGGATATA CAACAACAAG	1620
CTGCATCACA CACTATAACA AAGGATATTG TTTTCATATA GTAGAAATAA ATCAGAAAAG	1680
CTTAAACACA CTTCAACCCA TGTTGTTCAA GACAGAGGTT CCAAAAAGCT GCAGTTAATC	1740
ATAATTAACC GCAATATGCA TTAACCTATC TATAATACAA GTATATGATA AGTAATCAGC	1800
AATCAGACAA TAGACAAAAG GGAAATATAA AAA	1833

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 572 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Glu	Tyr	Trp	Lys	His	Thr	Asn	His	Gly	Lys	Asp	Ala	Gly	Asn	Glu
1				5					10					15	

Leu	Glu	Thr	Ser	Met	Ala	Thr	Asn	Gly	Asn	Lys	Leu	Thr	Asn	Lys	Ile
			20					25					30		

Thr	Tyr	Ile	Leu	Trp	Thr	Ile	Ile	Leu	Val	Leu	Leu	Ser	Ile	Val	Phe
		35					40					45			

Ser Gln Val Asn Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys
515 520 525

Ser Asp Glu Leu Leu His Asn Val Asn Ala Gly Lys Ser Thr Thr Asn
530 535 540

Ile Met Ile Thr Thr Ile Ile Ile Glu Ile Ile Val Ile Leu Leu Ser
545 550 555 560

Leu Ile Ala Val Gly Leu Leu Leu Tyr Cys Lys Ala Arg Ser Thr Pro
565 570 575

Val Thr Leu Ser Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile Ala Phe
580 585 590

Ser Asn

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 920 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGCAAACATG	TCCAAAAACA	AGGACCAACG	CACCGCTAAG	ACACTAGAAA	AGACCTGGGA	60
CACTCTCAAT	CATTTATTAT	TCATATCATC	GGGCTTATAT	AAGTTAAATC	TTAAATCTGT	120
AGCACAAATC	ACATTATCCA	TTCTGGCAAT	GATAATCTCA	ACTTCACTTA	TAATTACAGC	180
CATCATATTC	ATAGCCTCGG	CAAACCACAA	AGTCACACTA	ACAACTGCAA	TCATACAAGA	240
TGCAACAAGC	CAGATCAAGA	ACACAACCCC	AACATACCTC	ACTCAGGATC	CTCAGCTTGG	300
AATCAGCTTC	TCCAATCTGT	CTGAAATTAC	ATCACAAACC	ACCACCATAC	TAGCTTCAAC	360
AACACCAGGA	GTCAAGTCAA	ACCTGCAACC	CACAACAGTC	AAGACTAAAA	ACACAACAAC	420
AACCCAAACA	CAACCCAGCA	AGCCCACTAC	AAAACAACGC	CAAAACAAAC	CACCAAACAA	480
ACCCAATAAT	GATTTTCACT	TCGAAGTGTT	TAACTTTGTA	CCCTGCAGCA	TATGCAGCAA	540
CAATCCAACC	TGCTGGGCTA	TCTGCAAAAG	AATACCAAAC	AAAAAACCAG	GAAAGAAAAC	600
CACCACCAAG	CCTACAAAAA	AACCAACCTT	CAAGACAACC	AAAAAAGATC	TCAAACCTCA	660
AACCACTAAA	CCAAAGGAAG	TACCCACCAC	CAAGCCCACA	GAAGAGCCAA	CCATCAACAC	720

Lys Pro Gly Lys Lys Thr Thr Thr Lys Pro Thr Lys Lys Pro Thr Phe
 195 200 205
 Lys Thr Thr Lys Lys Asp Leu Lys Pro Gln Thr Thr Lys Pro Lys Glu
 210 215 220
 Val Pro Thr Thr Lys Pro Thr Glu Glu Pro Thr Ile Asn Thr Thr Lys
 225 230 235 240
 Thr Asn Ile Thr Thr Thr Leu Leu Thr Asn Asn Thr Thr Gly Asn Pro
 245 250 255
 Lys Leu Thr Ser Gln Met Glu Thr Phe His Ser Thr Ser Ser Glu Gly
 260 265 270
 Asn Leu Ser Pro Ser Gln Val Ser Thr Thr Ser Glu His Pro Ser Gln
 275 280 285
 Pro Ser Ser Pro Pro Asn Thr Thr Arg Gln
 290 295

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATCAATCAAA GGTCCTGTGA TAATAG

26

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CATGACTTGA TAATGAG

17

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 86 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

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ATTTCTGTGA TATTTGTGCG GTATAATGAT GCTATACCT

39

(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

CAGGAGAAGG GTATCAAG

18

(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

AGGAGAAGGG TATCAAG

17

(A) LENGTH: 94 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

ATCATGGAGA TAATTAAAAT GATAACCATC TCGCAAATAA ATAAGTATTT TACTGTTTTTC

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gln Glu Lys Gly Ile Lys

1 5

(2) INFORMATION FOR SEO ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Gln Glu Lys Gly Ile Lys

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(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATCAATCTAG CACTACACAG

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1617 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1715 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATGGAATACT	GGAAGCATAC	CAATCACGGA	AAGGATGCTG	GCAATGAGCT	GGAGACGTCC	60
ATGGCTACTA	ATGGCAACAA	GCTCACCAAT	AAGATAACAT	ATATATTATG	GACAATAATC	120
CTGGTGTTAT	TATCAATAGT	CTTCATCATA	GTGCTAATTA	ATTCCATCAA	AAGTGAAAAG	180
GCTCATGAAT	CATTGCTGCA	AGACATAAAT	AATGAGTTTA	TGGAAATTAC	AGAAAAGATC	240
CAAATGGCAT	CGGATAATAC	CAATGATCTA	ATACAGTCAG	GAGTGAATAC	AAGGCTTCTT	300
ACAATTCAGA	GTCATGTCCA	GAATTATATA	CCAATATCAC	TGACACAACA	GATGTCAGAT	360
CTTAGGAAAT	TCATTAGTGA	AATTACAATT	AGAAATGATA	ATCAAGAAGT	GCTGCCACAA	420
AGAATAACAC	ATGATGTGGG	TATAAAACCT	TTAAATCCAG	ATGATTTTTG	GAGATGCACG	480
TCTGGTCTTC	CATCTTTAAT	GAAAACTCCA	AAAATAAGGT	TAATGCCAGG	GCCGGGATTA	540
TTAGCTATGC	CAACGACTGT	TGATGGCTGT	ATCAGAACTC	CGTCCTTAGT	TATAAATGAT	600
CTGATTTATG	CTTATACCTC	AAATCTAATT	ACTCGAGGTT	GTCAGGATAT	AGGAAAATCA	660
TATCAAGTCT	TACAGATAGG	GATAATAACT	GTAAACTCAG	ACTTGGTACC	TGACTTAAAT	720
CCCAGGATCT	CTCATACTTT	TAACATAAAT	GACAATAGGA	AGTCATGTTC	TCTAGCACTC	780
CTAAATACAG	ATGTATATCA	ACTGTGTTCA	ACTCCCAAAG	TTGATGAAAG	ATCAGATTAT	840
GCATCATCAG	GCATAGAAGA	TATTGTACTT	GATATTGTCA	ATTATGATGG	CTCAATCTCA	900
ACAACAAGAT	TTAAGAATAA	TAACATAAGC	TTTGATCAAC	CTTATGCTGC	ACTATACCCA	960
TCTGTTGGAC	CAGGGATATA	CTACAAAGGC	AAAATAATAT	TTCTCGGGTA	TGGAGGTCTT	1020
GAACATCCAA	TAAATGAGAA	TGTAATCTGC	AACACAACCTG	GGTGTCCCGG	GAAAACACAG	1080
AGAGACTGCA	ATCAGGCATC	TCATAGTCCA	TGGTTTTTCAG	ATAGGAGGAT	GGTCAACTCT	1140
ATCATTGTTG	TTGACAAAGG	CTTAAACTCA	ATTCCAAAAT	TGAAGGTATG	GACGATATCT	1200
ATGAGACAGA	ATTACTGGGG	GTCAGAAGGA	AGGTTACTTC	TACTAGGTAA	CAAGATCTAT	1260
ATATATACAA	GATCCACAAG	TTGGCATAGC	AAGTTACAAT	TAGGAATAAT	TGATATTACT	1320
GATTACAGTG	ATATAAGGAT	AAAATGGACA	TGGCATAATG	TGCTATCAAG	ACCAGGAAAC	1380

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CTATGTACAA CCAACACAAA AGAAGGGTCA AACATCTGTT TAACAAGAAC TGACAGAGGA	1020
TGGTACTGTG ACAATGCAGG ATCAGTATCT TTCTTCCCAC AAGCTGAAAC ATGTAAAGTT	1080
CAATCGAATC GAGTATTTTG TGACACAATG AACAGTTTAA CATTACCAAG TGAAGTAAAT	1140
CTCTGCAATG TTGACATATT CAATCCCCAA TATGATTGTA AAATTATGAC TTCAAAAACA	1200
GATGTAAGCA GCTCCGTTAT CACATCTCTA GGAGCCATTG TGTCATGCTA TGGCAAAACT	1260
AAATGTACAG CATCCAATAA AAATCGTGGA ATCATAAAGA CATTTTCTAA CGGGTGTGAT	1320
TATGTATCAA ATAAAGGGGT GGACACTGTG TCTGTAGGTA ACACATTATA TTATGTAAAT	1380
AAGCAAGAAG GCAAAAGTCT CTATGTAAAA GGTGAACCAA TAATAAATTT CTATGACCCA	1440
TTAGTATTCC CCTCTGATGA ATTTGATGCA TCAATATCTC AAGTCAATGA GAAGATTAAC	1500
CAGAGTTTAG CATTTATTCG TAAATCCGAT GAATTATTAC ATAATGTAAA TGCTGGTAAA	1560
TCAACCACAA ATATCATGAT AACTACTATA ATTATAGTGA TTATAGTAAT ATTGTTATCA	1620
TTAATTGCTG TTGGACTGCT CCTATACTGT AAGGCCAGAA GCACACCAGT CACACTAAGC	1680
AAGGATCAAC TGAGTGGTAT AAATAATATT GCATTTAGTA AC	1722

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 894 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATGTCCAAAA ACAAGGACCA ACGCACCGCT AAGACACTAG AAAAGACCTG GGACACTCTC	60
AATCATTTAT TATTCATATC ATCGGGCTTA TATAAGTTAA ATCTTAAATC TGTAGCACAA	120
ATCACATTAT CCATTCTGGC AATGATAATC TCAACTTCAC TTATAATTAC AGCCATCATA	180
TTCATAGCCT CGGCAAACCA CAAAGTCACA CTAACAACCTG CAATCATACA AGATGCAACA	240
AGCCAGATCA AGAACACAAC CCCAACATAC CTCACTCAGG ATCCTCAGCT TGGAATCAGC	300
TTCTCCAATC TGTCTGAAAT TACATCACAA ACCACCACCA TACTAGCTTC AACAAACACCA	360
GGAGTCAAGT CAAACCTGCA ACCCACAACA GTCAAGACTA AAAACACAAC AACAAACCCAA	420
ACACAACCCA GCAAGCCCAC TACAAAACAA CGCCAAAACA AACCACCAAA CAAACCCAAT	480
AATGATTTTC ACTTCGAAGT GTTTAACTTT GTACCCTGCA GCATATGCAG CAACAATCCA	540

[illegible]

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

27

(2) INFORMATION FOR SEO ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTACGGTTGA	AATTATGACG	ATTAATAATG	TTGTTACTAA	TACCGTAGAA	GGACGGTTTA	60
TCTATAGTGT	TTTGATGTCG	TACATCCACA	TAACCAGTTG	TCAGGGTTTC	CCTACTTCTA	120
TAGTGTTTTG	AAGCTT					136

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 98 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TAGTACCTCT ATTAATTTTA CTATTGGTAG AGCGTTTATT TATTCATAAA ATGACAAAAG 60

CATTGTCAAA ACATTATTTT TTTGGATATT TATCTTAA 98

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

AGGACAAAAG

10

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